

SEQUENCE LISTING

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<120> Novel cytochrome P450 monooxygenases and their use for the oxidation of organic substrates

<130> 50915

<140> 10/031,146

<141> Filing date not yet granted

<150> PCT/EP 00/07253

<151> 2000-07-27

<160> 9

<170> Word Perfect version 6.1

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His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val Gln		
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His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp Gln		
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 <223> Description of the synthetic sequence: PCR primer

<400> 3

gcaggagacg gggtggnnac aagctggacg

30

<210> 4
 <211> 30
 <212> DNA
 <213> Synthetic sequence

<220>
 <221> unsure
 <222> 1..30
 <223> n is g, a, t or c.

<223> Description of the synthetic sequence: PCR primer

<400> 4

10

cgtccagctt gttnncaacc cgtctcctgc

30

<210> 5
<211> 34
<212> DNA
<213> Synthetic sequence

<220>
<221> unsure
<222> 1..34
<223> n is g, a, t or c.

<223> Description of the synthetic sequence: PCR primer

<400> 5
gaagcaatga acaagnnnca gcgagcaaatt ccag

34

<210> 6
<211> 30
<212> DNA
<213> Synthetic sequence

<220>
<221> unsure
<222> 1..30
<223> n is g, a, t or c.

<223> Description of the synthetic sequence: PCR primer

<400> 6
ctggatttgc tcgctgnnnc ttgttcattg

30

<210> 7
<211> 41
<212> DNA
<213> Synthetic sequence

<220>
<221> unsure
<222> 1..41
<223> n is g, a, t or c.

<223> Description of the synthetic sequence: PCR primer

<400> 7

gctttgataa aaacttaaag tcaannnctt aaatttgtac g

41

<210> 8
<211> 40
<212> DNA
<213> Synthetic sequence

<220>
<221> unsure
<222> 1..40
<223> n is g, a, t or c.

<223> Description of the synthetic sequence: PCR primer

40

cgtacaaatt taagnnnttg acttaagttt ttatcaaagc

<211> 1049

<213> Bacillus megaterium

Met Thr Ile Lys Glu Met Pro Gln Pro Lys Thr Phe Gly Glu Leu Lys
1 5 10 15

Asn Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys
20 25 30

Ile Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg
35 40 45

Val Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp
50 55 60

Glu Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg
65 70 75 80

Asp Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn
85 90 95

Trp Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala
100 105 110

Met Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val
115 120 125

Gln Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu
130 135 140

Asp Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn
145 150 155 160

Tyr Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr
165 170 175

Ser Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala
180 185 190

Asn Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu
195 200 205

Asp Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg
210 215 220

Lys Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn
225 230 235 240

Gly Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg
245 250 255

12

Tyr Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly
 260 265 270
 Leu Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu
 275 280 285
 Gln Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro
 290 295 300
 Ser Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn
 305 310 315 320
 Glu Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala
 325 330 335
 Lys Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp
 340 345 350
 Glu Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp
 355 360 365
 Gly Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser
 370 375 380
 Ala Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala
 385 390 395 400
 Cys Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly
 405 410 415
 Met Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu
 420 425 430
 Asp Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys
 435 440 445
 Ala Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr
 450 455 460
 Glu Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn
 465 470 475 480
 Thr Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly
 485 490 495
 Thr Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro
 500 505 510
 Gln Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly
 515 520 525
 Ala Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn
 530 535 540
 Ala Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val
 545 550 555 560
 Lys Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala
 565 570 575

Thr Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala
 580 585 590
 Lys Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp
 595 600 605
 Asp Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp
 610 615 620
 Val Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys
 625 630 635 640
 Ser Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu
 645 650 655
 Ala Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu
 660 665 670
 Leu Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu
 675 680 685
 Leu Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile
 690 695 700
 Pro Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly
 705 710 715 720
 Leu Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu
 725 730 735
 Ala His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln
 740 745 750
 Tyr Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met
 755 760 765
 Ala Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu
 770 775 780
 Leu Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr
 785 790 795 800
 Met Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser
 805 810 815
 Glu Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile
 820 825 830
 Ser Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser
 835 840 845
 Val Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile
 850 855 860
 Ala Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys
 865 870 875 880
 Phe Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu

14

885										890					895				
Thr	Pro	Leu	Ile	Met	Val	Gly	Pro	Gly	Thr	Gly	Val	Ala	Pro	Phe	Arg				
			900					905					910						
Gly	Phe	Val	Gln	Ala	Arg	Lys	Gln	Leu	Lys	Glu	Gln	Gly	Gln	Ser	Leu				
		915					920					925							
Gly	Glu	Ala	His	Leu	Tyr	Phe	Gly	Cys	Arg	Ser	Pro	His	Glu	Asp	Tyr				
	930					935					940								
Leu	Tyr	Gln	Glu	Glu	Leu	Glu	Asn	Ala	Gln	Ser	Glu	Gly	Ile	Ile	Thr				
945					950					955					960				
Leu	His	Thr	Ala	Phe	Ser	Arg	Met	Pro	Asn	Gln	Pro	Lys	Thr	Tyr	Val				
				965					970					975					
Gln	His	Val	Met	Glu	Gln	Asp	Gly	Lys	Lys	Leu	Ile	Glu	Leu	Leu	Asp				
			980					985					990						
Gln	Gly	Ala	His	Phe	Tyr	Ile	Cys	Gly	Asp	Gly	Ser	Gln	Met	Ala	Pro				
		995					1000					1005							
Ala	Val	Glu	Ala	Thr	Leu	Met	Lys	Ser	Tyr	Ala	Asp	Val	His	Gln	Val				
	1010					1015					1020								
Ser	Glu	Ala	Asp	Ala	Arg	Leu	Trp	Leu	Gln	Gln	Leu	Glu	Glu	Lys	Gly				
1025					1030				1035					1040					
Arg	Tyr	Ala	Lys	Asp	Val	Trp	Ala	Gly											
				1045															